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(54) Title: INFECTIOUS BURSAL DISEASE VIRUS RECOMBINANT POXVIRUS VACCINE		
(57) Abstract		
What is described is a recombinant poxvirus, such as fowlpox virus, containing foreign DNA from infectious bursal disease virus. What is also described is a vaccine containing the recombinant poxvirus for inducing an immunological response in a host animal inoculated with the vaccine.		

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INFECTIOUS BURSAL DISEASE VIRUS

RECOMBINANT POXVIRUS VACCINE

CROSS REFERENCE TO RELATED APPLICATIONS

This application is a continuation-in-part of
5 copending application Serial No. 07/736,254 filed July
26, 1991, incorporated herein by reference. Reference is
also made to copending application Serial No. 07/847,951,
filed March 6, 1992, also incorporated herein by
reference.

10 FIELD OF THE INVENTION

The present invention relates to a modified
poxvirus and to methods of making and using the same.
More in particular, the invention relates to recombinant
poxvirus, which virus expresses gene products of an
15 infectious bursal disease virus (IBDV) gene, and to
vaccines which provide protective immunity against IBDV
infections.

Several publications are referenced in this
application. Full citation to these documents is found
20 at the end of the specification preceding the claims.
These documents pertain to the field of this invention;
and, each of the documents referenced in this application
are hereby incorporated herein by reference.

BACKGROUND OF THE INVENTION

25 Vaccinia virus and more recently other
poxviruses have been used for the insertion and
expression of foreign genes. The basic technique of
inserting foreign genes into live infectious poxvirus
involves recombination between pox DNA sequences flanking
30 a foreign genetic element in a donor plasmid and
homologous sequences present in the rescuing poxvirus
(Piccini et al., 1987).

Specifically, the recombinant poxviruses are
constructed in two steps known in the art and analogous
35 to the methods for creating synthetic recombinants of the
vaccinia virus described in U.S. Patent Nos. 5,110,587,
4,769,330, 4,722,848, and 4,603,112; the disclosures of

each of these patents is incorporated herein by reference. Reference is also made to copending application Serial No. 07/537,890, filed June 14, 1990, also incorporated herein by reference.

5 First, the DNA gene sequence to be inserted into the virus, particularly an open reading frame from a non-pox source, is placed into an *E. coli* plasmid construct into which DNA homologous to a section of DNA of the poxvirus has been inserted. Separately, the DNA
10 gene sequence to be inserted is ligated to a promoter. The promoter-gene linkage is positioned in the plasmid construct so that the promoter-gene linkage is flanked on both ends by DNA homologous to a DNA sequence flanking a region of pox DNA containing a nonessential locus. The
15 resulting plasmid construct is then amplified by growth within *E. coli* bacteria (Clewell, 1972) and isolated (Clewell et al., 1969; Sambrook et al., 1989).

Second, the isolated plasmid containing the DNA gene sequence to be inserted is transfected into a cell
20 culture, e.g. chick embryo fibroblasts, along with the poxvirus. Recombination between homologous pox DNA in the plasmid and the viral genome respectively gives a poxvirus modified by the presence, in a nonessential region of its genome, of foreign DNA sequences. The term
25 "foreign" DNA designates exogenous DNA, particularly DNA from a non-pox source, that codes for gene products not ordinarily produced by the genome into which the exogenous DNA is placed.

Genetic recombination is in general the
30 exchange of homologous sections of DNA between two strands of DNA. In certain viruses RNA may replace DNA. Homologous sections of nucleic acid are sections of nucleic acid (DNA or RNA) which have the same sequence of nucleotide bases.

35 Genetic recombination may take place naturally during the replication or manufacture of new viral genomes within the infected host cell. Thus, genetic

recombination between viral genes may occur during the viral replication cycle that takes place in a host cell which is co-infected with two or more different viruses or other genetic constructs. A section of DNA from a 5 first genome is used interchangeably in constructing the section of the genome of a second co-infecting virus in which the DNA is homologous with that of the first viral genome.

However, recombination can also take place 10 between sections of DNA in different genomes that are not perfectly homologous. If one such section is from a first genome homologous with a section of another genome except for the presence within the first section of, for example, a genetic marker or a gene coding for an 15 antigenic determinant inserted into a portion of the homologous DNA, recombination can still take place and the products of that recombination are then detectable by the presence of that genetic marker or gene in the recombinant viral genome.

Successful expression of the inserted DNA 20 genetic sequence by the modified infectious virus requires two conditions. First, the insertion must be into a nonessential region of the virus in order that the modified virus remain viable. The second condition for 25 expression of inserted DNA is the presence of a promoter in the proper relationship to the inserted DNA. The promoter must be placed so that it is located upstream from the DNA sequence to be expressed.

The technology of generating vaccinia virus 30 recombinants has recently been extended to other members of the poxvirus family which have a more restricted host range. The avipox virus, fowlpox, has been engineered as a recombinant virus. This recombinant virus is described in PCT Publication No. WO89/03429, also incorporated 35 herein by reference.

Fowlpox virus (FPV) has advantageously been engineered as a vector expressing antigens from poultry

pathogens. The hemagglutinin protein of a virulent avian influenza virus was expressed in an FPV recombinant (Taylor et al., 1988). After inoculation of the recombinant into chickens and turkeys, an immune response 5 was induced which was protective against either a homologous or heterologous virulent influenza virus challenge (Taylor et al., 1988). In addition, the surface glycoproteins (fusion and hemagglutinin) of a virulent strain of Newcastle Disease Virus have been 10 expressed in an FPV vector and shown to induce a protective immune response (Taylor et al., 1990; Edbauer et al., 1990).

FPV is the prototypic virus of the Avipox genus of the Poxvirus family. The virus causes an economically 15 important disease of poultry which has been well controlled since the 1920's by the use of live attenuated vaccines. Replication of the avipox viruses is limited to avian species (Matthews, 1982) and there are no reports in the literature of the virus causing a 20 productive infection in any non-avian species including man. This host restriction provides an inherent safety barrier to transmission of the virus to other species and makes use of FPV as a vaccine vector in poultry an attractive proposition.

25 Infectious bursal disease, also known as Gumboro's disease, manifests itself in two ways. In chickens older than three weeks, infectious bursal disease virus (IBDV) can cause impaired growth and mortality losses of up to 20% (Lukert and Hitchner, 30 1984). In younger birds, the disease is subclinical but is evident as microscopic lesions in the bursa of Fabricius (Winterfield et al., 1972). This results in prolonged and severe immunosuppression which causes increased susceptibility to disease and interferes with 35 vaccination programs against other disease agents (Allan et al., 1972). Characteristics of the disease have been

reviewed in Lukert and Saif (1991) and will be summarized briefly here.

The cloacal bursa appears to be the primary target organ of the virus and birds surgically bursectomized at 4 weeks have been shown to survive a lethal IBDV challenge without clinical manifestations (Kaufer and Weis, 1980). The age of bursectomy is however, critical. Schat et al., (1981) performed embryonal bursectomy and then challenged with IBDV at 2 and 6 weeks of age. Birds developed typical hemorrhagic lesions, were clinically ill and showed some mortality. The target cells are actively dividing B lymphocytes (Muller, 1986; Burkhardt and Muller, 1987). Muller (1986) demonstrated that IBDV will replicate preferentially in lymphoid cells from the bursa and poorly in lymphoid cells from other organs. It has been proposed that clinical signs of IBDV infection may result from immune complex formation (Ley et al., 1979; Skeeles et al., 1979). Muller (1986) however, demonstrated that the preferential replication in the lymphoid cells of the bursa is not related to the presence of surface immunoglobulins.

Two serotypes of IBDV, designated 1 and 2 have been demonstrated (McFerran et al., 1980; Jackwood et al., 1984; McNulty and Saif, 1988). Virulent serotypes have been shown in Group 1. No disease has been associated with group 2 viruses. In addition, considerable antigenic variation has been documented within serotypes (Lukert and Saif, 1991).

The causative agent, IBDV, has been classified as a Birnavirus (Brown et al., 1986). The biochemistry and replication of IBDV has been reviewed in Kibenge et al., (1988). Birnaviruses are small non-enveloped animal viruses having two segments of double-stranded RNA. The smaller genomic segment (segment B) of IBDV encodes a single polypeptide of 90k designated VP1. This protein is a minor internal component of the virion and is

presumed to be the viral RNA polymerase (Hudson et al., 1986; Nagy et al., 1987; Spies et al., 1987). The larger genomic segment (segment A) encodes 5 polypeptides with the following designations and approximate molecular weights 52k (VPX), 41k (VP2), 32k (VP3), 28k (VP4) and 16k (Azad et al., 1985). The identity and presence of the 16K polypeptide has not been confirmed (Kibenge et al., 1988). VP2, VP3 and VP4 arise by co-translational proteolytic cleavage of precursor polyproteins. The protein VP4 is thought to be a viral protease (Hudson et al., 1986) responsible for cleavage between VPX and VP4 (Duncan et al., 1987) and between VP4 and VP3 (Azad et al., 1987; Jagadish et al., 1988).

Protein VP2 is the most abundant protein of the viral capsid making up 51% of serotype I IBDV proteins (Dobos et al., 1979). VP2 is only found in mature viral particles and is not seen in IBDV infected cells (Becht et al., 1988). VP2 is thought to be a specific cleavage product of a VPX precursor. Peptide mapping has shown that VPX and VP2 of IBDV strain CU-1 have similar amino acid sequences (Muller and Becht, 1982; Dobos, 1979). In addition both VPX and VP2 react with the same monoclonal antibody on Western blots (Fahey et al., 1985b; Becht et al., 1988). It has recently been demonstrated that a conformational dependent neutralizing epitope exists on VP2 (Azad et al., 1987; Fahey et al., 1989) and a conformation independent neutralizing epitope exists on VP3 (Fahey et al., 1985 a,b). Antibodies to these epitopes were found to passively protect chickens (Fahey et al., 1985b; Azad et al., 1987; Fahey et al. 1989). Becht et al., (1988) and Snyder et al., (1988) indicated that neutralizing monoclonal antibodies to VP2 differentiated between serotypes 1 and 2 in cross-neutralization tests. However, Becht et al., (1988) also indicated that monoclonal antibodies to VP3 recognized a group-specific antigen from both serotypes which was not associated with neutralizing activity or protection.

These studies may indicate the existence of multiple epitopes at least on VP2 and perhaps on VP3.

In a recent publication, Macreadie et al., (1990) demonstrated the expression of VP2 in a yeast vector. The size of the expressed protein was consistent with that of an authentic VP2. Centrifugation and gel filtration studies indicated that the VP2 expressed in yeast was in a high molecular weight aggregated form. Chickens inoculated with a crude extract of the yeast expressed VP2 developed an immune response as demonstrated by ELISA test and virus neutralization tests. One day old chickens were then inoculated with anti-sera from chickens previously inoculated with yeast expressed VP2. These chickens were passively protected against IBDV challenge as evidenced by lack of IBDV antigen in the bursa (Macreadie et al., 1990).

Current vaccination strategies against IBDV include both live and killed vaccines. Antibody transmitted from the hen via the yolk of the egg can protect chickens against early infections with IBDV. Therefore, use of killed vaccines in oil emulsions to stimulate high levels of maternal antibody is extensive in the field (Lukert and Saif, 1991). Studies by Lucio and Hitchner (1979) and Baxendale and Luttkien (1981) indicated that oil emulsion IBDV vaccines can stimulate adequate maternal immunity to protect chickens for 4-6 weeks. In contrast progeny from breeders vaccinated with live vaccines are protected for only 1-3 weeks after hatching (Lukert and Saif, 1991).

Determination of when maternal antibody has waned, and thus when antibody levels can be boosted by active immunization is problematical. It is therefore common practice to vaccinate all chicks against IBD with a live vaccine during the first 3 weeks of life (Winterfield et al., 1980). Inactivated vaccines are ineffective in inducing active immunity in chicks with maternal antibody. Presently available live vaccines

consist of strains of intermediate virulence or highly attenuated strains, as well as some cell culture adapted variant strains. While intermediate strains can break through maternal antibody titers of approximately 1:250 (Lukert and Saif, 1991), the strains vary in virulence and can induce bursal atrophy and immunosuppression in day old and 3 week old SPF chickens (Lukert and Mazariegos, 1985).

Given the limitations of current vaccination strategies, it can be appreciated that provision of an IBDV recombinant poxvirus, and of vaccines which provide protective immunity against IBDV infections, would be a highly desirable advance over the current state of technology.

OBJECTS OF THE INVENTION

It is therefore an object of this invention to provide recombinant poxviruses, which viruses express gene products of IBDV, and to provide a method of making such recombinant poxviruses.

It is an additional object of this invention to provide for the cloning and expression of IBDV coding sequences, particularly sequences coding for IBDV structural proteins, in a poxvirus vector, particularly fowlpox virus.

It is another object of this invention to provide a vaccine which is capable of eliciting IBDV antibodies and protective immunity against IBDV infection.

These and other objects and advantages of the present invention will become more readily apparent after consideration of the following.

STATEMENT OF THE INVENTION

In one aspect, the present invention relates to a recombinant poxvirus containing therein a DNA sequence from IBDV in a nonessential region of the poxvirus genome. The poxvirus is advantageously an avipox virus, such as fowlpox virus.

According to the present invention, the recombinant poxvirus expresses gene products of the foreign IBDV gene. In particular, the foreign DNA codes for IBDV structural proteins. The IBDV gene may be co-expressed with other foreign genes in the host by the recombinant poxvirus.

In another aspect, the present invention relates to a vaccine for inducing an immunological response in a host animal inoculated with the vaccine, said vaccine including a carrier and a recombinant poxvirus containing, in a nonessential region thereof, DNA from IBDV. Advantageously, the DNA codes for and expresses IBDV structural proteins. The IBDV gene may be co-expressed with other foreign genes in the host. The poxvirus used in the vaccine according to the present invention is advantageously an avipox virus, such as fowlpox virus, referred to hereafter as TROVAC.

BRIEF DESCRIPTION OF THE DRAWINGS

A better understanding of the present invention will be had by referring to the accompanying drawings, in which:

FIG. 1 (SEQ ID NO:7) shows the nucleotide sequence of a 3661 base pair fragment of TROVAC DNA containing the F8 open reading frame; and

FIG. 2 (SEQ ID NO:12) shows the nucleotide sequence of a 3659 base pair fragment of TROVAC DNA containing the F8 open reading frame.

DETAILED DESCRIPTION OF THE INVENTION

The invention is directed to recombinant poxviruses containing therein a DNA sequence from IBDV in a nonessential region of the poxvirus genome. The recombinant poxviruses express gene products of the foreign IBDV gene. In particular, IBDV genes encoding IBDV structural proteins were isolated, characterized and inserted into TROVAC (FPV) recombinants.

Cell Lines and Virus Strains. The strain of FPV designated FP-1 has been previously described (Taylor

et al., 1988). It is an attenuated vaccine strain useful in vaccination of day old chickens. The parental virus strain Duvette was obtained in France as a fowlpox scab from a chicken. The virus was attenuated by 5 approximately 50 serial passages in chicken embryonated eggs followed by 25 passages on chicken embryo fibroblast (CEF) cells. This virus was obtained in September 1980 by Rhone Merieux, Lyon, France and a master viral seed established. Subsequently, the virus was subjected to 10 four successive plaque purifications. One plaque isolate was further amplified in primary CEF cells, and a stock virus, designated as TROVAC, established.

CDNA clones from IBDV strain Faragher (Type I) were obtained from Rhone Merieux, Lyon, France.

15 Example 1 - CONSTRUCTION OF INSERTION VECTOR FOR IBDV-VP2

Plasmid pIBDVA contains a 3.1 Kb KpnI to XbaI fragment derived from cDNA clones of IBDV strain Faragher. This fragment was inserted into vector 20 pBluescript II SK+ (Stratagene, La Jolla, CA). The insert corresponds to the segment A of the IBDV genome which encodes the 108 kDa precursor polyprotein. The polyprotein is subsequently processed to form VP2, VP3 and VP4.

25 In order to isolate the coding sequence for VP2 from pIBDVA, VP3 and VP4 coding sequences were deleted from pIBDVA and a termination codon added to the 3' end of the VP2 coding sequence. This was accomplished by digestion of pIBDVA with ScaI and KpnI and insertion of 30 the annealed and kinased oligonucleotides CE279 (SEQ ID NO:1) and CE280 (SEQ ID NO:2) to form pCEN112.

CE279

ACTTCATGGAGGTGGCCGACCTCAACTCTCCCTGAAGATTGCAGGAGCATT
TGGCTTCAAAGACATAATCCGGGCTATAAGGAGGTGAGTCGACGGTAC

35 CE280

CGTCGACTCACCTCCTTATAGCCGGATTATGTCTTGAAAGCCAAATGCTCC
TGCAATCTTCAGGGGAGAGTTGAGGTCGCCACCTCCATGAAGT

The vaccinia virus H6 promoter previously described in Taylor et al., (1988); Guo et al., (1989), Perkus et al., (1989), was inserted into pCEN112 by digesting pCEN112 with NotI, and blunt-ending with the 5 Klenow fragment of DNA polymerase, in the presence of 10 mM dNTPs. A HindIII to EcoRV fragment which contains the H6 promoter was blunt-ended with the Klenow fragment of DNA polymerase and inserted into the linearized pCEN112 to generate pCEN117.

10 In order to couple the promoter sequence with the initiating ATG of IBDV VP2 coding sequence, the annealed and kinased oligonucleotides CE277 (SEQ ID NO:3) and CE278 (SEQ ID NO:4) were inserted into pCEN117 that had been digested with NruI and RsrII. The resulting 15 plasmid was designated pCEN120.

CE277

CGATATCATGACAAACCTGCAAGATCAAACCCAACAGATTGTTCCGTTTCATA
CGGAGCCTTCTGATGCCAACAAACCG

CE278

20 GTCCGGTTGTTGGCATCAGAAGGCTCCGTATGAACGGAACAATCTGTTGGGT
TTGATCTTGCAGGTTGTATGATATCG

A SmaI to SalI fragment from pCEN120, containing IBDV-VP2 linked to the vaccinia virus H6 promoter was cloned into the HpaI and SalI sites of the 25 FPV insertion vector pCEN100 (described below) to generate pCEN137. Plasmid pCEN137 was used in an *in vitro* recombination test to generate recombinant vFP115.

Example 2 - CONSTRUCTION OF INSERTION VECTOR FOR IBDV VP2, VP3, VP4

30 Non-coding sequence was removed from the 3' end of the IBDV polyprotein sequence by partially digesting pIBDVA with PpuMI, completely digesting with KpnI, and re-inserting the annealed and kinased oligonucleotides CE275 (SEQ ID NO:5) and CE276 (SEQ ID NO:6) into pIBDVA 35 to generate pCEN111.

CE275: GACCTTGAGTGAGTCGACGGTAC

CE276: CGTCGACTCACTCAAG

A perfect 5' end to the polyprotein sequence was obtained in the following manner. A KpnI-BstEII fragment containing the majority of the polyprotein sequence with a perfect 3' end was excised from pCEN111 5 and ligated into the KpnI and BstEII sites of pCEN120. This substitution replaces the 3' end of the VP2 coding sequence and generates a perfect 5' end for the polyprotein with linkage to the vaccinia virus H6 promoter. The resulting plasmid was designated pCEN125.

10 The final insertion plasmid was constructed by partial digestion of pCEN125 with SmaI and complete digestion with SalI. The resulting fragment was cloned into the HpaI and SalI sites of pCEN100 (described below) to form pCEN138. Plasmid pCEN138 was used in an *in vitro* 15 recombination test to generate recombinant vFP116.

Example 3 - CONSTRUCTION OF FOWLPOX INSERTION PLASMID AT F8 LOCUS

Plasmid pRW731.15 contains a 10 Kbp PvuII-PvuII fragment cloned from TROVAC genomic DNA. The nucleotide 20 sequence was determined on both strands for a 3661 bp PvuII-EcoRV fragment. This sequence is shown in Figure 1 (SEQ ID NO:7). The limits of an open reading frame designated in this laboratory as F8 were determined within this sequence.

25 Subsequently, the nucleotide sequence of Fig. 1 was further analyzed and was determined on both strands to be a 3659 bp PvuII-EcoRV fragment. This sequence is shown in Figure 2 (SEQ ID NO:12). The limits of the open reading frame designated in this laboratory as F8 were 30 determined within this sequence; and, the subsequent determination of the sequence, as shown in Fig. 2, does not affect the reproducibility of this or any other construction involving the fowlpox F8 locus determined by this laboratory, especially because the deletions and 35 insertions into the F8 ORF can be performed by the skilled artisan following the teachings from this laboratory, such as the following description, without

recourse to the sequence of the F8 ORF or the PvuII-EcoRV fragment within which it is contained. Based on sequence information contained in Figure 2, the open reading frame is initiated at position 495 and terminates at position 5 1887. A deletion was engineered from what was ultimately determined to be position 779 to position 1926, as described below.

Plasmid pRW761 is a sub-clone of pRW731.15 containing a 2430 bp EcoRV-EcoRV fragment. Plasmid 10 pRW761 was completely digested with XbaI and partially digested with SspI. A 3700 bp XbaI-SspI band was isolated and ligated with the annealed double-stranded oligonucleotides JCA017 (SEQ ID NO:8) and JCA018 (SEQ ID NO:9).

15 JCA017 5' CTAGACACTTATGTTTTAATATCCGGTCTTAAAGCTTCCCGGG
GGATCCTTATAACGGGAATAAT 3'
JCA018 5' ATTATTCCCCGTATAAGGATCCCCGGGAAGCTTTAAGACCGGATA
TTAAAAAACATAAAGTGT 3'

The plasmid resulting from this ligation was 20 designated pJCA002.

Additional cloning sites were incorporated into pJCA002 by inserting the annealed and kinased oligonucleotides CE205 (SEQ ID NO:10) and CE206 (SEQ ID NO:11) into the BamHI and HindIII sites of pJCA002 to 25 form pCE72.

CE205: GATCAGAAAAACTAGCTAGTAGTACGTAGTTAACGTCGACCTGCAG
AAGCTTCTAGCTAGCTAGTTTTAT

CE206: AGCTATAAAAATAGCTAGCTAGAAGCTTCTGCAGGTCGACGTTAAC
TACGTACTAGCTAGCTAGTTTTCT

30 In order to increase the length of the FPV flanking arms in the insertion plasmid, plasmid pJCA021 was constructed. Plasmid pJCA021 was obtained by inserting a 4900bp PvuII-HindII fragment from pRW731.15 (described above) into the SmaI and HindII sites of 35 pBluescript SK+ (Stratagene, La Jolla, CA). A BglII to EcoRI fragment from pCE72 was then ligated into the BglII and EcoRI sites of pJCA021 to generate pCE100.

Example 4 - DEVELOPMENT OF TROVAC-IBDV RECOMBINANTS

Plasmids pCEN137 and pCEN138 were transfected into TROVAC infected primary CEF cells by using the calcium phosphate precipitation method previously described (Panicali and Paoletti, 1982; Piccini et al., 1987). Positive plaques were selected on the basis of hybridization to specific IBDV radiolabeled probes and subjected to five sequential rounds of plaque purification until a pure population was achieved. One representative plaque from each IVR was then amplified and the resulting TROVAC recombinants were designated vFP115 (IBDV-VP2) and vFP116 (IBDV-VP2, VP3, VP4).

Immunofluorescence. In order to determine where the IBDV proteins were localized in recombinant infected CEF cells, immunofluorescence analysis was performed. Indirect immunofluorescence was performed as described in Taylor et al., (1990) using a neutralizing monoclonal antibody preparation specific for VP2 and designated AC6 and a VP3 specific monoclonal antibody designated NA3 obtained from Rhone Merieux. In addition, a polyclonal chicken anti-IBDV serum was obtained from Spafas Inc., Storrs, CT.

The results indicated that IBDV specific immunofluorescence could be detected in the cytoplasm of cells infected with either vFP115 or vFP116. No fluorescence was detected in parental TROVAC infected CEF cells. No surface fluorescence was detected in cells infected with either recombinant virus. Equivalent results were obtained using both the neutralizing monoclonal antibody preparation and the polyclonal immune serum. The result was not unexpected since the analysis of the sequence of the IBDV genes does not indicate the presence of characteristic signal and anchor sequences which would direct insertion of the proteins in the infected cell membrane.

Immunoprecipitation. Immunoprecipitation reactions were performed as described in Taylor et al.,

(1990) using the monoclonal antibody preparations and the polyclonal anti-IBDV immune serum from chickens as described above.

Immunoprecipitation analysis of CEF cells

- 5 infected with recombinant vFP115 indicated the expression of a protein of approximately 38-40 Kd recognized by both polyclonal immune sera and the neutralizing monoclonal antibody. This size is appropriate for expression of the structural protein, VP2 (Azad et al., 1985).
- 10 Immunoprecipitation analysis of lysates of cells infected with recombinant vFP116 encoding the IBDV polyprotein, with the same serological reagents, also demonstrated expression of a single protein species of approximately 43 kd. This protein is recognized by both polyclonal
- 15 immune serum and the neutralizing monoclonal antibody preparation. Both the size of the protein and its recognition by the monoclonal antibody indicate that the identity of this protein may be VPX, the precursor to VP2. Although no other proteins are immunoprecipitated
- 20 by the polyclonal immune serum, presence of the cleaved VPX indicates that VP4, the cleavage protein is probably expressed. Since VP4 is a very minor component of the virion, it is not unusual that the immune serum should not contain antibodies to this protein. Use of the VP3
- 25 specific monoclonal antibody indicated the expression of a protein of 32 kd in cells infected with vFP116.

Example 5 - IMMUNIZATION OF CHICKENS AND SUBSEQUENT CHALLENGE

- Groups of 20, 5 day old susceptible SPF
- 30 chickens were inoculated by subcutaneous injection in the nape of the neck with 0.2 ml of recombinants vFP115 or vFP116. This corresponded to a dose of approximately 4.0 \log_{10} TCID₅₀. A group of 19 birds were left as uninoculated controls. At fourteen days post
- 35 vaccination, chickens were bled and serum neutralizing titers in the sera were determined. Birds were challenged at 14 days by intra-ocular inoculation of 0.03

ml of the virulent heterologous serotype I IBDV challenge strain (designated STC) supplied by the USDA National Veterinary Services Laboratory. Five days after challenge, each chicken was necropsied and the bursa examined for gross lesions and the appearance of atrophy.

5 The results are shown in Table 1.

The results indicate that inoculation of one dose of vFP115 expressing the VP2 structural protein leads to the induction of serum neutralizing antibody and

10 75% protection of challenged birds. Inoculation of vFP116 leads to the induction of a poor neutralizing antibody response but 50% of challenged birds are protected.

TABLE 1. Protective Efficacy of TROVAC-IBDV Recombinants in Chickens

	Recombinant	#Protected/ Challenged ^b	% Protection	SN Titer ^a
20	vFP115	15/20	75	131
	vFP116	10/19	53	6
	Controls	0/19	0	0

a: Serum neutralization titer

25 b: Birds are considered protected in the absence of bursal atrophy and lesions.

Example 6 - IBDV RECOMBINANT POXVIRUS VACCINES

Recombinant poxviruses containing, in a nonessential region thereof, DNA from IBDV provide

30 advantages as vaccines for inducing an immunological response in a host animal. Infectious bursal disease virus is very stable and persists in the environment for long periods. For economic reasons, poultry houses are rarely cleaned between broods and thus chickens are

35 exposed to the virus early in life. Since elimination of virus by hygienic means is not possible, vaccination strategies need to be formed. Active immunization of

chickens is difficult in the presence of maternal antibody. In addition, since maternal antibody levels are variable and the rate of loss of antibody unpredictable, timing of vaccination is a problem. A successful vaccine will need to be able to boost immunity in the presence of maternal antibody and should also contain cross-reactive antigens from a number of different serotypes. In addition, an effective vaccine should not induce signs of disease in vaccinated birds.

TROVAC-IBDV recombinant vFP115 expressed the major structural protein VP2 which has been shown to contain at least one highly immunogenic region. The protein expressed by the TROVAC recombinant is recognizable by IBDV immune serum. Inoculation of this recombinant into susceptible birds resulted in 75% protection from bursal damage. Recombinant vFP116 contains the coding sequence for the polyprotein VP2, VP3, VP4. A protein probably corresponding to VPX, the VP2 precursor, was expressed which is also recognized by IBDV immune sera. Inoculation of this recombinant into susceptible birds lead to the development of low neutralizing antibody levels, but induced 53% protection from bursal damage.

The results indicate the potential of TROVAC-IBDV recombinants for vaccination against IBDV in the poultry industry. The restricted host range of FPV provides an inherent safety barrier to transmission of recombinant to non-vaccinated species. Use of antigenic regions of IBDV rather than whole virus eliminates the need to introduce live virus to the environment and may lessen the immunological pressure on the virus which leads to the emergence of variant strains. The large size of the FPV genome allows incorporation of multiple antigenic sequences and should allow for vaccination against a variety of strains.

Example 7 - FURTHER IMMUNOGENICITY AND EFFICACY STUDIES WITH vFP115

Effect of dose of inoculation on protective efficacy induced by vFP115. Groups of day old SPF chickens were inoculated with vFP115 by the subcutaneous route in the nape of the neck. The virus was

5 administered in doses of 4.9, 5.5 or 6.2 log₁₀ EID₅₀ per bird. At 21 days post-vaccination, ten vaccines and ten naive birds were bled and the sera analyzed for the presence of IBDV specific serum neutralizing (SN) antibody. At 28 days, birds were challenged by

10 administration by the ocular route of 1.3 log₁₀ EID₅₀ of the heterologous Standard Challenge Strain of IBDV. At 5 days post-challenge, 5 birds from each group were necropsied and bursae examined for gross lesions. At 11 days post-challenge, the remaining birds were killed and

15 bursa to body weight ratios determined. The results of analysis are shown in Table 2. The results indicate that increasing the inoculation dose has led to the induction of slightly higher levels of SN antibody, but that the protective efficacy is not enhanced. Birds were

20 considered protected when the bursa to body weight ratio after challenge was greater than one standard deviation of the mean bursa to body weight ratio of infected control birds. Using this criteria, and considering bursa to body weight ratios of individual birds,

25 protection ratios of 65%, 74% and 64% were obtained for vFP115 dosages of 4.9, 5.5 and 6.2 log₁₀ EID₅₀ respectively.

TABLE 2. Dose Response Study of Inoculation of vFP115 in Day Old Chickens

Dose 5	SN GMT ^a	Bursal Lesions ^b	Bursa/Body Weight
		Positive/Total	Ratio ^c
4.9	13	1/5	3.5
5.5	35	2/5	3.2
6.2	102	1/5	3.2
10 Control	0	5/5	1.6

a: Geometric Mean Titer of sera of 10 birds

b: Bursa of 5 birds examined for gross lesions

c: Ratio expressed as a mean of 23 birds

15

Effect of Age of Bird on Protective Efficacy of vFP115. Groups of 30 one-, four-, seven- and fourteen day old SPF birds were inoculated by the subcutaneous route with $4.0 \log_{10}$ EID₅₀ of vFP115. At 21 days post-vaccination, 10 vaccines and 5 naive controls of each group were bled and sera analyzed for the presence of SN antibody. At 28 days post-vaccination, all vaccines and naive controls were challenged by the ocular route with $1.3 \log_{10}$ EID₅₀ of the heterologous STC virus strain. Four days post-challenge, birds were sacrificed and bursa examined for evidence of bursal damage. The results of analysis are shown in Table 3. The results indicate that while IBD specific SN titers and protection after challenge are obtained at one day of age, when vaccination is delayed past 4 days of age higher SN titers are obtained and the level of protection is increased.

35

TABLE 3. Effect of Age of Bird on Protective Efficacy of vFP115

Age 5 Group	Treatment	GMT	Protection	%
			Ratio	Protection
1 day	Vaccinates	126	23/30	77
	Controls		0/10	0
4 days	Vaccinates	666	25/30	83
	Controls		0/10	0
10	Vaccinates	1946	29/30	97
	Controls		1/10	0
14 days	Vaccinates	1408	30/30	100
	Controls		0/10	0

15 Effect of route of inoculation on induction of a protective immune response by vFP115. Groups of twenty 14 day old SPF birds were inoculated by (a) the intramuscular route in the leg, (b) ocular route or (c) 20 oral route with $4.0 \log_{10}$ TCID₅₀ of vFP115. At 14 and 28 days post-inoculation sera were collected and analyzed for the presence of IBDV specific SN antibody. At both 14 and 28 days post-vaccination, groups of birds were challenged by ocular inoculation of $2.5 \log_{10}$ EID₅₀ of the 25 homologous Faragher strain of IBDV. Deaths were recorded and at 4 days post-challenge all birds were sacrificed and Bursa examined for the presence of macroscopic lesions. Significant neutralizing antibody responses were found only after inoculation of vFP115 by the 30 intramuscular route with SN titers of approximately 2.0 \log_{10} at 14 and 28 days post-inoculation. By ocular and oral routes, low SN titers were achieved in 30 and 10% of chickens, respectively. The results of challenge are shown in Table 4. All birds inoculated with vFP115 by 35 the intramuscular route were fully protected from challenge which was pathogenic in all control non-vaccinated birds at 14 and 28 days post-inoculation. No

protection was observed following the oral route of inoculation. Partial protection was seen by the ocular route.

TABLE 4. Effect of Route of Inoculation on Protective Efficacy Induced By vFP115

Route of Inoculation	% Protection from challenge at	
	14 days post-vacc.	28 days post-vacc
10 Intramuscular	100	100
Ocular	50	10
Oral	0	0

Example 8 - DEVELOPMENT OF A TROVAC RECOMBINANT EXPRESSING THE VP3 STRUCTURAL PROTEIN

Example 2 describes the development of a TROVAC based recombinant vFP116 expressing the VP2, VP4, VP3 polyprotein. Efficacy studies described in Example 5 indicate that this recombinant induces lower levels of protection than vFP115 expressing the VP2 protein after inoculation into susceptible chickens. In vitro studies showed that the VP2 protein expressed in the vFP116 construct is slightly larger than that expressed in the vFP115 construct and that expression of the VP3 protein is not detectable by a polyclonal serum.

Immunofluorescence and immunoprecipitation analysis with a VP3 specific monoclonal antibody, however, indicated that the VP3 protein is expressed in vFP116. In order to evaluate the role of the VP3 protein in eliciting cross-protective immunity, a single recombinant was developed expressing the VP3 protein from the Faragher strain of IBDV.

Construction of a Fowlpox Insertion Plasmid at the F16 Locus. The plasmid pFP23K (described by Tartaglia et al., 1990) contains a 10.5 kb HindIII fragment from the fowlpox (FP) genome. A 7.3 kb NaeI\NdeI FP fragment was isolated from pFP23K and

ligated to a similarly cut pUC9 vector to generate pRW866. A unique FspI site within this FP fragment lies between two ORFs (intergenic region) and is the F16 insertion locus.

5 In order to create a multiple cloning site (MCS) cassette for the F16 locus, two PCR fragments were amplified from pFP23K using primers RW264 (SEQ ID NO:13) plus RW265 (SEQ ID NO:14) and RW266 (SEQ ID NO:15) plus RW267 (SEQ ID NO:16). The resulting fragments were mixed
10 together and amplified with primers RW266 and RW267 which resulted in a single, fused fragment. This fragment was digested with EcoRI and NdeI and ligated into similarly cut pRW715 (derived from pUC9 by digesting with PvuII and ligating an EcoRI linker between the two PvuII sites), to
15 yield pRW864. The MCS cassette consists of a polycloning region (SmaI-BamHI-HindIII sites) flanked on either side by translational stop codons in all six reading frames and a NotI site. A vaccinia early transcriptional stop signal is located on the HindIII end.

20 RW264: AATTAACCCGGGATCCAAGCTTAGCTAGCTAATTTT
ATAGCGGCCGCTATAATCGTTAACCTATTAG
RW265: CTAGCTAGAACGTTGGATCCC GGTTAATTAATTAATAAAAAA
GC GGCC CGCTTAAAGTAGAAAAATG
RW266: GTTACATATGTACAGAATCTGATCATAG
25 RW267: GCTAGAATTCTCTTAGTTTTATAGTTG

The following describes a series of plasmid constructs which ultimately leads to the MCS cassette from pRW864 being inserted into the FspI site of pRW866 to generate the F16 insertion plasmid (pRW873). A
30 cassette containing the *E. coli* lacZ gene coupled to the vaccinia 11K promoter was excised from pAM1BG as a BamHI/PstI fragment. Plasmid pAM1BG contains the lacZ BamHI fragment from pMC1871 (Casadaban et al., 1983) inserted in the previously described BamHI site 3' of the
35 11K vaccinia virus promoter (Paoletti et al., 1984). The ends were repaired using Klenow polymerase and the cassette ligated into pRW864 cut with SmaI to yield

pRW867A. The lacZ gene cassette was excised from pRW867A using NotI and the ends repaired with Klenow polymerase. This fragment was then ligated into the unique FspI site in the FP sequences of pRW866 resulting in pRW868. The 5 lacZ gene from pRW868 was excised using NotI and replaced with the MCS cassette derived as a NotI fragment from pRW864 resulting in pRW873, the F16 insertion plasmid.

Development of an FP recombinant expressing VP3. The complete IBDV VP3 ORF was excised from pCEN111 10 (described in Example 3) as a 1262 bp BamHI and Asp718 fragment and ligated into a similarly cut pSD554VC (a vaccinia donor plasmid containing the H6 promoter) to yield pFT1. A 112 bp PCR fragment was amplified from pCEN111 using oligonucleotides JP003 (SEQ ID NO:17) and 15 JP004 (SEQ ID NO:18), digested with NruI/ScaI, and gel purified. This fragment was ligated into pFT1 digested completely with NruI and partially with ScaI to yield pIBDV-VP3II. This plasmid contains the vaccinia H6 promoter coupled to the VP3 ORF.

20 A PCR fragment was amplified from pRW823 which contains vaccinia virus H6 promoter sequences using oligonucleotides RG662 (SEQ ID NO:19) and RG663 (SEQ ID NO:20). This fragment was digested with HindIII/SmaI and ligated into the F16 insertion plasmid (pRW873) cut with 25 the same enzymes resulting in pF16VQH6. A cassette containing part of the H6 promoter fused to the VP3 ORF was excised from pIBDV-VP3II with NruI/Asp718, the ends repaired with Klenow polymerase, and the purified fragment ligated into pF16VQH6 cut with NruI/SmaI to 30 generate the donor plasmid pF16VP3F.

JP003 5'-AAGGTAGTACTGGCGTCC-3'

JP004 5'-TTATCGCGATATCCGTTAAGTTGTATCGTAATATGTTCCCTCACAA-
ATCCACGA-3'

RG662 5'-TAAAAGCTTTAATTAAATTAGTCATC-3'

35 RG663 5'-TAACCCGGCGATAACAACTTAACGG-3'

Plasmid pF16VP3F was used in *in vitro* recombination with TROVAC as the rescuing virus to derive

recombinant vFP186. Immunoprecipitation analysis using a VP3 specific monoclonal antibody has confirmed the expression of a protein of approximately 32 kd in CEF cells infected with the recombinant.

5 Example 9 - DEVELOPMENT OF TROVAC BASED RECOMBINANTS WITH ALTERED MODES OF EXPRESSION OF THE VP2 PROTEIN

It has been postulated that a protein displayed on the infected cell surface may lead to a more efficient 10 induction of neutralizing antibody than if the protein is secreted or expressed internally. Previous studies have indicated that expression of a foreign antigen on the infected cell surface by a recombinant vaccinia virus, can be achieved by recombinant DNA techniques by adding 15 appropriate signal and anchor sequences (Langford et al., 1986; Vijaya et al., 1988). The VP2 protein in IBDV infected cells is not a membrane bound glycoprotein and possesses neither an endogenous signal nor anchor 20 sequences. A strategy was devised to add the appropriate signal and anchor sequences from the Newcastle Disease Virus fusion protein. The fusion protein is an integral membrane bound glycoprotein. This strategy is described below.

The IBDV VP2 ORF plus translational stop codon 25 was excised from pCEN112 (described in Example 1) as an XbaI/Sall fragment and the ends repaired using Klenow polymerase. This cassette was ligated into the HincII site of pUC18 to generate pCE147. The vaccinia H6 promoter coupled to the NDV fusion gene signal sequence 30 was obtained by isolating a HindIII/PstI fragment from pCE64 (for complete NDV Fusion sequences see Taylor et al., 1990). This fragment contains the H6 promoter fused to the first 25 codons from the N-terminus of the NDV fusion ORF. This fragment was ligated into pCE147 cut 35 with HindIII/PstI to yield pCEN150.

In order to couple the last codon from the NDV fusion signal sequence with the first codon from the VP2

ORF, a PCR fragment was amplified from pCEN150 using oligonucleotides CE329 (SEQ ID NO:21) and CE330 (SEQ ID NO:22) as primers. The fragment was digested with KpnI/RsrII and ligated into pCEN150 cut with the same enzymes to generate pCEN156. The H6 promoted-NDV fusion signal sequence-VP2 ORF cassette was excised from pCEN156 with HindIII/EcoRI, the ends repaired using Klenow polymerase, and the cassette ligated into pCEN100 (the F8 insertion plasmid) cut with HpaI to generate the donor plasmid pIBDV-VP2-SS.

CE329 5'-GATCCGGTACCTCTAATGCTGATCATCCGAACCGCGCTGACACTG-
AGCTGTACAAACCTGCAAGATCAAAC-3'

CE330 5'-GGACGCCGGTCCGGTTGTTGGCATC-3'

To add the NDV fusion transmembrane sequences to the above plasmid, a 240 bp PCR fragment was amplified from pIBDV-VP2-SS using primers RG583 (SEQ ID NO:23) and RG590 (SEQ ID NO:24). This fragment contains 49 codons plus stop codon from the C-terminus of the NDV fusion ORF (see Taylor et al., 1990). The purified fragment was digested with ScaI/BamHI and ligated into pIBDV-VP2-SS cut completely with BamHI and partially with ScaI to generate the donor plasmid pIBDV-VP2-SSA.

RG583 5'-GTGAGTACTTCATGGAGGTGGCCGACCTCAACTCTCCCCTGAAGA-
TTGCAGGAGCATTGGCTCAAAGACATAATCCGGGCTATAAGGA-
25 GGATCGTTTAACGTGTCATATC-3'

RG590 5'-TTAGGATCCTCATATTTGTAGTGGCTCTC-3'

In vitro recombination using plasmid pIBDV-VP2-SS and TROVAC as the rescuing virus generated recombinant vFP147. Expression analysis of this recombinant with both polyclonal immune serum and a VP2 specific monoclonal antibody indicated that the VP2 protein is expressed internally, and in addition is secreted into the tissue culture fluid. This result is in keeping with the addition of a signal sequence to the coding sequence of the VP2 protein. *In vitro* recombination using plasmid pIBDV-VP2-SSA and TROVAC as the rescuing virus generated recombinant vFP151. Expression analysis using both

polyclonal immune serum and the VP2 specific monoclonal antibody indicated that the VP2 protein is expressed at the infected cell surface as expected following the addition of an anchor sequence. The fact that the VP2 protein is still recognized by the monoclonal antibody in this form of presentation indicates that conformation of this particular epitope has not been altered by the manipulations.

Efficacy studies were performed by inoculating 10 day-old SPF chickens with $4.0 \log_{10} \text{TCID}_{50}$ of each recombinant. At 28 days birds were challenged by ocular inoculation of the heterologous STC challenge strain. In contrast to previous results obtained with the unmodified VP2 expressed in vFP115, no protection was obtained after 15 vaccination with either vFP147 or vFP151. Further *in vitro* studies using tunicamycin, an inhibitor of N-linked glycosylation, have indicated that the modified VP2 proteins expressed by both vFP147 and vFP151 are glycosylated whereas the unmodified VP2 expressed in vFP115 is not. It is postulated that the addition of sugar moieties to the VP2 protein may alter conformation of the protein in areas apart from the neutralizing epitope. Alternatively, the addition of the signal and anchor sequences as constructed here, may alter 25 conformation of the protein. In either case it appears that the antibody induced by the modified constructions is not able to neutralize the heterologous challenge virus (STC). However, vFP147 and vFP151 and products therefrom are nonetheless useful. The modified VP2 30 expressed by these recombinants can be used as precursors to generate the VP2 protein; for example, by removal of the additional sugar moieties or to isolate secreted VP2 protein from tissue culture supernatant for further purification.

35 Example 10 - DEVELOPMENT OF POXVIRUS RECOMBINANTS
EXPRESSING THE VP2 PROTEIN FROM
HETEROLOGOUS STRAINS OF IBDV

IBDV strains show considerable variation in their ability to cross-neutralize. Sequence analysis of different strains has shown that one critical region involved in virus neutralization resides within a 5 conformational epitope located on VP2. Sequence information for VP2 is available for the Faragher (Bayliss et al., 1990) and STC (Kibenge et al., 1990) strains and it has been determined that five amino acid differences between the two strains occur within the 10 conformational epitope. A strategy was therefore devised to alter the coding sequence of the Faragher strain conformational epitope to conform with the sequence of the STC strain. This procedure is described below.

Mutagenesis of VP2 Faragher to VP2 STC. In 15 order to change the VP2 Faragher sequence in pCEN120 (described in Example 1) to the VP2 STC sequence, five codons were changed in the VP2 ORF using PCR site directed mutagenesis (see Kibenge et al., 1990 for STC sequence). Oligonucleotide primers RG677 (SEQ ID NO:25) 20 plus RG678 (SEQ ID NO:26) and RG685 (SEQ ID NO:27) plus RG686P (SEQ ID NO:28) were used to amplify a 530 bp and a 270 bp fragment respectively from pCEN100 (described in Example 3). The gel purified 270 bp fragment was further amplified using oligonucleotides RG702 (SEQ ID NO:29) and 25 RG704 (SEQ ID NO:30). The 530 bp fragment was digested with SacI and partially digested with PstI. The 270 bp fragment was digested with SacI and NcoI. These purified PCR amplified fragments, which contain the five STC codon changes, were ligated into pCEN120 cut with PstI and 30 NcoI. The resulting plasmid, pVP2-STC was confirmed by DNA sequencing analysis.

RG677 5'-TACACACTGCAGAGCAATGGAACCTCAAGTCGATCAGATG-3'
RG678 5'-GAAACACGAGCTCTCCCCAACGCTGAGGCTTGATAG-3'
RG685 5'-GGAAGAGCTCGTGTTCAAACAAGCGTCCAAGGCCTGTACTGGG-
35 CGCCACCACATCTACTTTATAGGCTTGATGGGACTACGGTAATCAC-
CAGAGCTGTAGCCGCAGATAATGGGCTGACGGCCGGCACCGACAA-
TCTTATGCCATTCAATCTTG-3'

RG686P 5'-CCACCATGGATCGTCACTGCTAGGCTCCCAC TTGCCGACC ATGAC-
ATCTGATCCCCCTGCCTGACC ACCACTTTGGAGGTCACTACCTCC-
AGTTGATGGATGTGATTGGCTGGGTTATCTCATTGGTTGGAATG-
ACAAGATTGAATGGCATAAG-3'

5 RG702 5'-GGGAGAGCTCGTGTTCAAACAAGCG-3'

RG704 5'-CCACCATGGATCGTCACTGC-3'

Construction of the new F8 insertion plasmid.

In order to remove all of F8 coding sequences from the original F8 insertion plasmid (pCEN100), a new F8 10 insertion plasmid was constructed. pJCA021 contains a 4900 bp PvuII/HincII fragment from TROVAC which includes the F8 gene and flanking sequences. A 4.2 kb NciI/PpuMI fragment was isolated from this plasmid and the ends repaired with Klenow polymerase. This fragment was 15 ligated into pBluescript SK+ cut with XbaI/Asp718 and repaired with Klenow polymerase to yield pIY.

The strategy to delete the F8 ORF from pIY and replace it with a multiple cloning site (MCS) used PCR amplification of two fragments from pJCA021 with 20 oligonucleotide primers containing the multiple cloning sequences. A 335 bp fragment was amplified from pJCA021 using oligonucleotides RG714 (SEQ ID NO:31) and RG715 (SEQ ID NO:32) and digested with HindIII and EcoRI. Similarly, a 465 bp fragment was amplified from pJCA021 25 using oligonucleotides RG716 (SEQ ID NO:33) and RG717 (SEQ ID NO:34) and digested with HindIII and BglII. The two PCR fragments were ligated into pIY cut with EcoRI and BglII in a three fragment ligation resulting in pF8. This plasmid is the new F8 insertion plasmid which 30 contains a MCS consisting of SmaI, NruI, HindIII, BamHI and XhoI sites flanked by vaccinia early transcriptional stop signals and translational stops in all six frames. The length of the left arm is about 1430 bp and the length of the right arm is about 1380 bp. The F8 gene 35 ORF which initiates at nucleotide position 495 and terminates at nucleotide position 1887 (Figure 2) is completely deleted.

29

- RG714 5'-AACATATTCGGAACAG-3'
RG715 5'-TCCAAGCTTCGCGACCCGGGTTTTATTAGCTAATTAGCAATAT-
AGATTCAATATG-3'
RG716 5'-ATCAAGCTTGGATCCCTCGAGTTTTATTGACTAGTTAACATAA-
5 GATAAAATAATATACAGC-3'
RG717 5'-GATATAGAAGATACCAG-3'

Construction of donor plasmids and recombinants
expressing VP2 STC. A cassette containing the H6
promoted VP2 (STC) ORF was excised as a 1.5 kb SmaI-
10 Asp718 fragment from pVP2-STC. The ends were repaired
using Klenow polymerase and ligated into pF8 cut with
SmaI to generate the pF8-STC donor plasmid.
Plasmid pF8-STC was used in *in vitro*
recombination with TROVAC as the rescuing virus to
15 generate recombinant vFP209. Expression analysis of the
recombinants using a polyclonal IBDV serum from chicken
indicated that the VP2 protein is expressed internally in
CEF cells infected by the recombinant.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Virogenetics Corporation

(ii) TITLE OF INVENTION: Infectious Bursal Disease Virus
Recombinant Poxvirus Vaccine

(iii) NUMBER OF SEQUENCES: 34

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

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(viii) ATTORNEY/AGENT INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ACTTCATGGA GGTGGCCGAC CTCAACTCTC CCCTGAAGAT TGCAGGGAGCA TTTGGCTTCA

60

AAGACATAAT CGGGCTATA AGGAGGTGAG TCGACGGTAC

100

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CGTCGACTCA CCTCCTTATA GCCCCGATTA TGTCTTGAA GCCAAATGCT CCTGCAATCT	60
TCAGGGGAGA GTTGAGGTCTG CCCACCTCCA TGAACT	96

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 77 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGATATCATG ACAAACCTGC AAGATCAAAC CCAACAGATT GTTCCGTTCA TACGGAGCCT	60
TCTGATGCCA ACAACCG	77

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 80 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTCCGGTTGT TGGCATCAGA AGGCTCCGTA TGAACGGAAC AATCTGTTGG GTTTGATCTT	60
GCAGGTTTGT CATGATATCG	80

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GACCTTGAGT GAGTCGACGG TAC	23
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(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CGTCGACTCA CTCAAG	16
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(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3661 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GATATCTGTG	GTCTATATAT	ACTACACCCT	ACCGATATTA	ACCAACGAGT	TTCTCACAAAG	60
AAAACCTTGT	TAGTAGATAG	AGATTCTTG	ATTGTGTTA	AAAGAAGTAC	CAGTAAAAAG	120
TGTGGCATAT	GCATAGAAGA	AATAAACAAA	AAACATATTT	CCGAACAGTA	TTTGGAATT	180
CTCCCAAGTT	GTAAACATAT	TTTTGCCTA	TCATGTATAA	GACGTTGGC	AGATACTACC	240
AGAAAATACAG	ATACTGAAAA	TACGTGTCCT	GAATGTAGAA	TAGTTTTCC	TTTCATAATA	300
CCCAGTAGGT	ATTGGATAGA	TAATAAATAT	GATAAAAAAA	TATTATATAA	TAGATATAAG	360
AAAATGATT	TTACAAAAAT	AACCTATAAG	AACAATAAAA	ATATAATTAC	ATTTACGGAA	420
AATAGCTGGT	TTTAGTTAC	CAACTTAGAG	TAATTATCAT	ATTGAATCTA	TATTGTTTT	480
TAGTTATATA	AAAACATGAT	TAGCCCCCAA	TCGGATGAAA	ATATAAAAGA	TGTTGAGAAT	540
TTCGAATACA	ACAAAAAGAG	GAATCGTACG	TTGTCCATAT	CCAAACATAT	AAATAAAAAT	600
TCAAAAGTAG	TATTACTG	GATGTTAGA	GATCAACGTG	TACAAGATAA	TTGGGCTTTA	660
ATTTACGCAC	AACGATTAGC	GTAAAACTC	AAAATACCTC	TAAGAATATG	CTTTGTGTC	720
GTGCCAAAT	TTCACACTAC	TACTTCTAGT	ACACTTATG	TTTTAATAT	CCGGTCTTAA	780
AGAAGTCGCG	GAAGAATGTA	AAAGACTATG	TATAGGGTTT	TCATTGATAT	ATGGCGTACC	840
AAAAGTAATA	ATTCCGTGTA	TAGTAAAAAA	ATACAGAGTC	GGAGTAATCA	TAACGGATT	900
CTTTCCATTA	CGTGTCCCCG	AAAGATTAAT	GAAACAGACT	GTATATCTC	TTCCAGATAA	960
CATACCTTT	ATACAAGTAG	ACGCTCATAA	TATAGTACCT	TGTTGGGAAG	CTTCTGATAA	1020
AGAAGAAATAC	GGTGCACGAA	CTTAAAGAAA	AAAGATATTT	GATAAATTAT	ATGAATATAT	1080
GACAGAATT	CCTGTTGTC	GTAAACATCC	ATACGGTCCA	TTTCTATAT	CTATTGCAA	1140
ACCCAAAAAT	ATATCATTAG	ACAAGACGGT	ATTACCCGTA	AAATGGCAA	CGCCTGGAAC	1200
AAAAGCTGGA	ATAATTGTT	AAAAGAATT	TATAAAAAAC	AGATTACCGT	CATACGACGC	1260
GGATCATAAC	AATCCTACGT	GTGACGCTTT	GAGTAACCTA	TCTCCGTGGC	TACATTTGG	1320
TCATGTATCC	GCACAACTG	TTGCCTTAGA	AGTATTAAAA	TGTATACGAG	AAAGCAAAA	1380
AAACGTTGAA	ACGTTTATAG	ATGAAATAAT	TGTAAGAAGA	GAACTATCGG	ATAATTTTG	1440
TTACTATAAC	AAACATTATG	ATAGTATCCA	GTCTACTCAT	TCATGGGTTA	AAAAAACATT	1500
AGAAGATCAC	ATTAATGATC	CTAGAAAGTA	TATATATTCC	ATTAACAAAC	TCGAAAAAGC	1560
GGAAAACAT	GATCCTCTAT	GGAACCGGTC	ACAAATGCAG	ATGGTGAGAG	AAGGAAAAAT	1620
GCATAGTTT	TTACGAATGT	ATTGGGCTAA	GAAGATACTT	GAATGGACTA	GAACACCTGA	1680
AGACGTTTG	AGTTATAGTA	TCTATTGAA	CAACAAGTAC	GAACTAGACG	GCACGGATCC	1740

TAACGGATAC GTAGGTTGTA TGTGGTCTAT TTGCGGATTAA CACGATAGAG CGTGGAAAGC	1800
AAGACCGATA TTTGGAAAGA TAAGATATAT GAATTATGAG AGTTCTAAGA AGAAATTGAA	1860
TGTTGCTGTA TTTATACAGA AATACAATTAA AGATAAATAA TATACAGCAT TGTAACCATC	1920
GTCATCCGTT ATACGGGGAA TAATATTACC ATACAGTATT ATTAAATTCTT CTTACGAAGA	1980
ATATAGATCG GTATTATCG TTAGTTTATT TTACATTAT TAATTAAACA TGTCTACTAT	2040
TACCTGTTAT GGAAATGACA AATTTAGTTA TATAATTAT GATAAAATTAA AGATAATAAT	2100
AATGAAATCA AATAATTATG TAAATGCTAC TAGATTATGT GAATTACGAG GAAGAAAGTT	2160
TACGAACTGG AAAAAATTAA GTGAATCTAA AATATTAGTC GATAATGTA AAAAAATAAA	2220
TGATAAAACT AACCAAGTTAA AAACCGATAT GATTATATAC GTTAAGGATA TTGATCATAA	2280
AGGAAGAGAT ACTTGCGGTT ACTATGTACA CCAAGATCTG GTATCTTCTA TATCAAATTG	2340
GATATCTCCG TTATTCGCCG TTAAGGTAAA TAAAATTATT AACTATTATA TATGTAATGA	2400
ATATGATATA CGACTTAGCG AAATGAAATC TGATATGACA GAAGTAATAG ATGTAGTTGA	2460
TAAATTAGTA GGAGGATACA ATGATGAAAT AGCAGAAATA ATATATTGT TTAATAAATT	2520
TATAGAAAAA TATATTGCTA ACATATCGTT ATCAACTGAA TTATCTAGTA TATTAAATTAA	2580
TTTTATAAAT TTTATAAATT TTAATAAAAAT ATACAATAAC GACATAAAGA TATTTAATCT	2640
TTAATTCTTG ATCTGAAAAA CACATCTATA AAAACTAGATA AAAAGTTATT CGATAAAGAT	2700
AATAATGAAT CGAACCGATGA AAAATTGGAA ACAGAAAGTT ATAAGCTAAT TTTTTTCATC	2760
TAAATAGTAT TATTTTATTG AAGTACGAAG TTTTACGTTA GATAAATAAT AAAGGTCGAT	2820
TTTTACTTTG TTAAATATCA AATATGTCA TATCTGATAA AGATACAAAA ACACACGGTG	2880
ATTATCAACC ATCTAACGAA CAGATATTAC AAAAAATACG TCGGACTATG GAAAACGAAG	2940
CTGATAGCCT CAATAGAAGA AGCATTAAAG AAATTGTTGT AGATGTTATG AAGAATTGGG	3000
ATCATCCTCA ACGAAGAAAT AGATAAAGTT CTAAACTGGA AAAATGATAC ATTAAACGAT	3060
TTAGATCATC TAAATACAGA TGATAATATT AAGGAAATCA TACAATGTCT GATTAGAGAA	3120
TTTGCCTTTA AAAAGATCAA TTCTATTATG TATAGTTATG CTATGGTAA ACTCAATTCA	3180
GATAACGAAC ATTGAAAGAT AAAATTAAGG ATTATTTAT AGAAAATCTT CTTAAAGACA	3240
AACGTGGTTA TAAACAAAAG CCATTACCCG GATTGGAAAC TAAAATACTA GATAGTATTA	3300
TAAGATTTA AAAACATAAA ATTAATAGGT TTTTATAGAT TGACTTATTA TATACAATAT	3360
GGATAAAAGA TATATATCAA CTAGAAAGTT GAATGACGGA TTCTTAATTT TATATTATGA	3420
TTCAATAGAA ATTATTGTCA TGTCGTGTA TCATTTTATA AATATATCAG CGTTACTAGC	3480
TAAGAAAAAC AAGGACTTTA ATGAATGGCT AAAGATAGAA TCATTTAGAG AAATAATAGA	3540
TACTTTAGAT AAAATTAATT ACGATCTAGG ACAACGATAT TGTGAAGAAC TTACGGCGCA	3600
TCACATTCCA GTGTAATTAT TGAGGTCAAA GCTAGTAACT TAATAGATGA CAGGACAGCT	3660
G	3661

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 69 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTAGACACTT TATGTTTTT AATATCCGGT CTTAAAGCT TCCCGGGGA TCCTTATAACG 60
GGGAATAAT 69

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 65 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATTATTCCCC GTATAAGGAT CCCCCGGGAA GCTTTAAGA CCGGATATTAA AAAAACATAA 60
AGTG 65

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 72 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GATCAGAAAA ACTAGCTAGC TAGTACGTAG TTAACGTCGA CCTGCAGAAG CTTCTAGCTA 60
GCTAGTTTT AT 72

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 72 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGCTATAAAA ACTAGCTAGC TAGAAGCTTC TGCAGGTCGA CGTTAACTAC GTACTAGCTA 60
GCTAGTTTT CT 72

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3659 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GATATCTGTG	GTCTATATAT	ACTACACCCT	ACCGATATTA	ACCAACGAGT	TTCTCACAAAG	60
AAAACTTGTT	TAGTAGATAG	AGATTCTTG	ATTGTGTTA	AAAGAAGTAC	CAGTAAAAAG	120
TGTGGCATAT	GCATAGAAGA	AATAAACAAA	AAACATATTT	CCGAACAGTA	TTTGGAATT	180
CTCCCAAGTT	GTAAACATAT	TTTTGCCTA	TCATGTATAA	GACGTTGGC	AGATACTACC	240
AGAAATACAG	ATACTGAAAA	TACGTGTCCT	GAATGTAGAA	TAGTTTTCC	TTTCATAATA	300
CCCAGTAGGT	ATTGGATAGA	TAATAAATAT	GATAAAAAAA	TATTATATAA	TAGATATAAG	360
AAAATGATT	TTACAAAAAT	ACCTATAAGA	ACAATAAAA	TATAATTACA	TTTACGGAAA	420
ATAGCTGGTT	TTAGTTACC	AACTTAGAGT	AATTATCATA	TTGAATCTAT	ATTGTTTTT	480
AGTTATATAA	AAACATGATT	AGCCCCAAT	CGGATGAAAA	TATAAAAGAT	GTTGAGAATT	540
TCGAATACAA	CAAAAAGAGG	AATCGTACGT	TGTCCATATC	CAAACATATA	AATAAAAATT	600
CAAAAGTAGT	ATTATACTGG	ATGTTTAGAG	ATCAACGTGT	ACAAGATAAT	TGGGCTTTAA	660
TTTACGCACA	ACGATTAGCG	TTAAAACCTCA	AAATACCTCT	AAGAATATGC	TTTGTGTCG	720
TGCCAAAATT	TCACACTACT	ACTTCTAGAC	ACTTTATGTT	TTTAATATCC	GGTCTTAAAG	780
AAGTCGCGGA	AGAATGTAAA	AGACTATGTA	TAGGGTTTTC	ATTGATATAT	GGCGTACCAA	840
AAGTAATAAT	TCCGTGTATA	GTAAAAAAAT	ACAGAGTCGG	AGTAATCATA	ACGGATTCT	900
TTCCATTACG	TGTTCCGAA	AGATTAATGA	AACAGACTGT	AATATCTCTT	CCAGATAACA	960
TACCTTTAT	ACAAGTAGAC	GCTCATAATA	TAGTACCTTG	TTGGGAAGCT	TCTGATAAAG	1020
AAGAAATACGG	TGCACCAA	ACT TTAAGAAAAA	AGATATTGAA	TAATTATAT	GAATATATGA	1080
CAGAATTTC	TGTTGTCGT	AAACATCCAT	ACGGTCCATT	TTCTATATCT	ATTGCAAAAC	1140
CCAAAAATAT	ATCATTAGAC	AAGACGGTAT	TACCCGTAAA	ATGGGCAACG	CCTGGAACAA	1200
AAGCTGGAAT	AATTGTTTA	AAAGAATTAA	TAACACAG	ATTACCGTCA	TACGACGCGG	1260
ATCATAACAA	TCCTACGTGT	GACGTTTGA	GTAACCTATC	TCCGTGGCTA	CATTTGGTC	1320
ATGTATCCGC	ACAACGTGTT	GCCTTAGAAG	TATTAAAATG	TATACGAGAA	AGCAAAAAAA	1380
ACGTTGAAAC	GTTTATAGAT	GAAATAATTG	TAAGAAGAGA	ACTATCGGAT	AATTTTGTT	1440
ACTATAACAA	ACATTATGAT	AGTATCCAGT	CTACTCATTC	ATGGGTTAGA	AAAACATTAG	1500
AAGATCACAT	TAATGATCCT	AGAAAGTATA	TATATTCCAT	AAACAACTC	AAAAAAGCGG	1560
AAACACTCATGA	TCCTCTATGG	AACGCGTCAC	AAATGCAGAT	GGTGAGAGAA	GGAAAAATGC	1620
ATAGTTTTT	ACGAATGTAT	TGGGCTAAGA	AGATACTTGA	ATGGACTAGA	ACACCTGAAG	1680

ACGCTTGAG TTATAGTATC TATTGAACA ACAAGTACGA ACTAGACGGC ACGGATCCTA	1740
ACGGATACGT AGGTTGTATG TGGTCTATT GC GGATTACA CGATAGAGCG TGAAAGCAA	1800
GACCGATATT TGGAAAGATA AGATATATGA ATTATGAGAG TTCTAAGAAG AAATTGATG	1860
TTGCTGTATT TATACAGAAA TACAATTAG ATAATAATA TACAGCATTG TAACCATCGT	1920
CATCCGTTAT ACGGGGAATA ATATTACCAT ACAGTATTAT TAAATTTCT TACGAAGAAT	1980
ATAGATCGGT ATTTATCGTT AGTTTATTTT ACATTTATA ATAAACATG TCTACTATTA	2040
CCTGTTATGG AAATGACAAA TTTAGTTATA TAATTTATGA TAAAATTAAG ATAATAATAA	2100
TGAAATCAAA TAATTATGTA AATGCTACTA GATTATGTGA ATTACGAGGA AGAAAGTTA	2160
CGAACTGGAA AAAATTAAGT GAATCTAAAA TATTAGTCGA TAATGTAAAA AAAATAATG	2220
ATAAAACTAA CCAGTTAAAA ACGGATATGA TTATATACGT TAAGGATATT GATCATAAAG	2280
GAAGAGATAC TTGCGGTTAC TATGTACACC AAGATCTGGT ATCTTCTATA TCAAATTGGA	2340
TATCTCCGTT ATTGCGCGTT AAGGTAAATA AAATTATTA CTATTATATA TGTAATGAAT	2400
ATGATATACG ACTTAGCGAA ATGGAATCTG ATATGACAGA AGTAATAGAT GTAGTTGATA	2460
AATTAGTAGG AGGATACAAT GATGAAATAG CAGAAATAAT ATATTGTTT AATAAATTAA	2520
TAGAAAATA TATTGCTAAC ATATCGTTAT CAACTGAATT ATCTAGTATA TTAAATAATT	2580
TTATAAATTAA TATAAATTAA AATAAAAAT ACAATAACGA CATAAAGATA TTTAATCTTT	2640
AATTCTTGAT CTGAAAAACA CATCTATAAA ACTAGATAAA AAGTTATTCG ATAAAGATAA	2700
TAATGAATCG AACGATGAAA AATTGGAAAC AGAAGTTGAT AAGCTAATTT TTTTCATCTA	2760
AATAGTATTA TTTTATTGAA GTACGAAGTT TTACGTTAGA TAAATAATAA AGGTCGATTT	2820
TTACTTTGTT AAATATCAA TATGTCATTA TCTGATAAAG ATACAAAAC ACACGGTGAT	2880
TATCAACCAT CTAACGAACA GATATTACAA AAAATACGTC GGACTATGGA AAACGAAGCT	2940
GATAGCCTCA ATAGAAGAAG CATTAAAGAA ATTGTTGTAG ATGTTATGAA GAATTGGGAT	3000
CATCCTCAAC GAAGAAATAG ATAAAGTTCT AACTGGAAA AATGATACAT TAAACGATTT	3060
AGATCATCTA AATACAGATG ATAATATTA GGAAATCATA CAATGTCTGA TTAGAGAATT	3120
TGCGTTAAA AAGATCAATT CTATTATGTA TAGTTATGCT ATGGTAAAC TCAATTCTAGA	3180
TAACGAACAT TGAAAGATAA ATTAAGGAT TATTTATAG AACTATTCT TAAAGACAAA	3240
CGTGGTTATA AACAAAAGCC ATTACCCGGA TTGGAAACTA AAATACTAGA TAGTATTATA	3300
AGATTTAAA AACATAAAAT TAATAGGTTT TTATAGATTG ACTTATTATA TACAATATGG	3360
ATAAAAGATA TATATCAACT AGAAAGTTGA ATGACGGATT CTTAATTTA TATTATGATT	3420
CAATAGAAAAT TATTGTCATG TCGTGTAAATC ATTTTATAAA TATATCAGCG TTACTAGCTA	3480
AGAAAAACAA GGACTTTAAT GAATGGCTAA AGATAGAATC ATTTAGAGAA ATAATAGATA	3540
CTTTAGATAA AATTAATTAC GATCTAGGAC AACGATATTG TGAAGAACTT ACGGCGCATC	3600
ACATTCCAGT GTAATTATTG AGGTCAAAGC TAGTAACCTA ATAGATGACA GGACAGCTG	3659

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 70 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AATTAACCCG GGATCCAAGC TTCTAGCTAG CTAATTAA TAGCGGCCGC TATAATCGTT

60

AACTTATTAG

70

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 67 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTAGCTAGAA GCTTGGATCC CGGGTTAATT AATTAATAAA AAGCGGCCGC GTTAAAGTAG

60

AAAAATG

67

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GTTACATATG TACAGAATCT GATCATAG

28

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCTAGAACCCG TCTTAGTTTT TATAGTTG

28

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AAGGTAGTAC TGGCGTCC

18

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 54 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTATCGCGAT ATCCGTTAAC TTTGTATCGT AATATGTTCC CTCACAATCC ACGA

54

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TAAAAGCTTT TAATTAATTA GTCATC

26

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TAACCCGGGC GATACAAACT TAACGG

26

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 72 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GATCCCGGTA CCTCTAATGC TGATCATCCG AACCGCGCTG ACACTGAGCT GTACAAACCT

60

GCAAGATCAA AC

72

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGACGCCGGT CCGGTTGTTG GCATC

25

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 112 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTGAGTACTT CATGGAGGTG GCCGACCTCA ACTCTCCCCT GAAGATTGCA GGAGCATTG

60

GCTTCAAAGA CATAATCCGG GCTATAAGGA GGATCGTTT AACTGTCATA TC

112

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TTAGGATCCT CATATTTTG TAGTGGCTCT C

31

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TACACACTGC AGAGCAATGG GAACCTCAAG TTGATCAGA TG

42

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GAAACACGAG CTCTCCCCCA ACGCTGAGGC TTGTGATAG

39

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 155 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GGAAGAGCTC GTGTTCAA CAAGCGTCCA AGGCCTTGTA CTGGCGCCA CCATCTACTT
 TATAGGCTTT GATGGGACTA CGGTAATCAC CAGAGCTGTA GCCGCAGATA ATGGGCTGAC
 GGCCGGCACC GACAATCTTA TGCCATTCAA TCTTG

60

120

155

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 155 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CCACCATGGA TCGTCACTGC TAGGCTCCC CTTGCCGACC ATGACATCTG ATCCCCTGCC
 TGACCACCA TTTGGAGGT CACTACCTCC AGTTTGATGG ATGTGATTGG CTGGGTTATC
 TCATTGGTTG GAATGACAAG ATTGAATGGC ATAAG

60

120

155

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGGAGAGCTC GTGTTCAA CAAGCG

26

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CCACCATGGA TCGTCACTGC

20

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AACATATTTC CGAACAG

17

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TCCAAGCTTT CGCGACCCGG GTTTTTATTA GCTAATTAGC AATATAGATT CAATATG

57

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATCAAGCTTG GATCCCTCGA GTTTTTATTG ACTAGTTAAT CATAAGATAA ATAATATACA

60

GC

62

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GATATAGAAG ATACCAG

17

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WHAT IS CLAIMED IS:

1. A recombinant poxvirus containing therein DNA from infectious bursal disease virus in a nonessential region of the poxvirus genome.
- 5 2. A recombinant poxvirus as in claim 1 wherein said DNA codes for and expresses an infectious bursal disease virus structural protein.
- 10 3. A recombinant poxvirus as in claim 2 wherein said structural protein is VP2.
4. A recombinant poxvirus as in claim 2 wherein said structural protein is polyprotein VP2, VP3, VP4.
- 15 5. A recombinant poxvirus as in claim 1 wherein the poxvirus is an avipox virus.
6. A recombinant avipox virus as in claim 6 wherein the avipox virus is fowlpox virus.
7. A recombinant fowlpox virus as in claim 7 20 which is selected from the group consisting of vFP115, vFP116, vFP147, vFP151, vFP186 and vFP209.
- 25 8. A vaccine for inducing an immunological response in a host animal inoculated with said vaccine, said vaccine comprising a carrier and a recombinant poxvirus containing, in a nonessential region thereof, DNA from infectious bursal disease virus.
9. A vaccine as in claim 9 wherein said DNA codes for and expresses an infectious bursal disease virus structural protein.
- 30 10. A vaccine as in claim 10 wherein said structural protein is VP2.
11. A vaccine as in claim 10 wherein said structural protein is VP3.
12. A vaccine as in claim 10 wherein said structural protein is polyprotein VP2, VP3, VP4.
- 35 13. A vaccine as in claim 9 wherein the poxvirus is an avipox virus.

14. A vaccine as in claim 14 wherein the avipox virus is fowlpox virus.

15. A vaccine as in claim 14 wherein the host animal is a chicken.

AMENDED CLAIMS

[received by the International Bureau on 14 December 1992 (14.12.92);
second claim 2 renumbered as claim 3,
original claims 3-15 renumbered as claims 4-16;
claim 1 unchanged (2 pages)]

1. A recombinant poxvirus containing therein DNA from infectious bursal disease virus in a nonessential region of the poxvirus genome.
- 5 2. A recombination poxvirus as in claim 1 wherein said DNA codes for and expresses an infectious bursal disease virus structural protein.
3. A recombinant poxvirus as in claim 2 wherein said structural protein is VP2.
- 10 4. A recombinant poxvirus as in claim 2 wherein said structural protein is VP3.
5. A recombinant poxvirus as in claim 2 wherein said structural protein is polyprotein VP2, VP3, VP4.
- 15 6. A recombinant poxvirus as in claim 1 wherein the poxvirus is an avipox virus.
7. A recombinant avipox virus as in claim 6 wherein the avipox virus is fowlpox virus.
- 20 8. A recombinant fowlpox virus as in claim 7 which is selected from the group consisting of vFP115, vFP116, vFP147, vFP151, vFP186 and vFP209.
9. A vaccine for inducing an immunological response in a host animal inoculated with said vaccine, said vaccine comprising a carrier and a recombinant
- 25 25 poxvirus containing, in a nonessential region thereof, DNA from infectious bursal disease virus.
10. A vaccine as in claim 9 wherein said DNA codes for and expresses an infectious bursal disease virus structural protein.
- 30 30 11. A vaccine as in claim 10 wherein said structural protein is VP2.
12. A vaccine as in claim 10 wherein said structural protein is VP3.
13. A vaccine as in claim 10 wherein said
- 35 35 structural protein is polyprotein VP2, VP3, VP4.
14. A vaccine as in claim 9 wherein the poxvirus is an avipox virus.

15. A vaccine as in claim 14 wherein the avipox virus is fowlpox virus.

16. A vaccine as in claim 14 wherein the host animal is a chicken.

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3/4

FIG. 1C

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1 GATATCTGTG GTCTATATAT ACTACACCCCT ACCGATATTAA ACCAACAGAGT TTCTCACAG
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 3601 ACATTCCAGT GTAATTATTG AGGTCAAAGC TAGTAACCTTA ATAGATGACA GGACAGCTG

FIG. 2

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US92/06100

A. CLASSIFICATION OF SUBJECT MATTER

IPC(5) :C12N 7/00; C12P 21/02; A61K 39/12

US CL :435/69.3, 235.1; 424/89

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/69.3, 235.1; 424/89

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
none

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

CAS ONLINE, search terms: poxvirus, infectious bursal disease virus, VP2, VP3, VP4

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	Azad et al. "Vaccines 90", published 1990 by Cold Spring Harbor Laboratory Press, CSH (NY), "Full Protection Against an Immunodepressive Viral Disease by a Recombinant Antigen Produced in Yeast", pages 59-62, entire document.	1, 2, 5, 6, 8
X,P	Archives of Virology, Volume 120, issued November 1991, C.D. Bayliss et al., "A Recombinant Fowlpox Virus that Expresses the VP2 Antigen of Infectious Bursal Disease Virus Induces Protection Against Mortality Caused by the Virus", pages 193-205, entire document.	1, 2, 5, 6, 8
Y	Virology, volume 161, issued October 1987, A.A. Azad et al., "Deletion Mapping and Expression in <u>Escherichia coli</u> of the Large Genomic Segment of a Birnavirus", pages 145-152, entire document.	1, 2, 5, 6, 8
Y	Nucleic Acids Research, Volume 14, No. 12, issued September 1986, P.J. Hudson et al., "Genomic Structure of the Large RNA Segment of Infectious Bursal Disease Virus", pages 5001-5012, entire document.	1, 2, 5, 6, 8

 Further documents are listed in the continuation of Box C. See patent family annex.

* Special categories of cited documents:	
"A"	document defining the general state of the art which is not considered to be part of particular relevance
"E"	earlier document published on or after the international filing date
"L"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O"	document referring to an oral disclosure, use, exhibition or other means
"P"	document published prior to the international filing date but later than the priority date claimed
"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"Z"	document member of the same patent family

Date of the actual completion of the international search

09 OCTOBER 1992

Date of mailing of the international search report

22 OCT 1992

Name and mailing address of the ISA/
Commissioner of Patents and Trademarks
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INTERNATIONAL SEARCH REPORT

International application No.

PCT/US92/06100

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Journal of General Virology, Volume 69, issued November 1988, F.S.B. Kibenge et al., "Biochemistry and Immunology of Infectious Bursal Disease Virus", pages 1757-1775, see especially page 1769.	1, 2, 5, 6, 8
Y	Journal of Virology, Volume 64, No. 4, issued April 1990, J. Taylor et al., "Newcastle disease Virus Fusion Protein Expressed in a Fowlpox Virus Recombinant Confers Protection in Chickens", pages 1441-1450, entire document.	1, 2, 5, 6, 8
Y	Vaccine, Volume 6, issued December 1988, J. Taylor et al. "Protective Immunity Against Avian Influenza Induced by a Fowlpox Virus Recombinant", pages 504-508, entire document.	1, 2, 5, 6, 8

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US92/06100

BOX I. OBSERVATIONS WHERE CLAIMS WERE FOUND UNSEARCHABLE**2. Where no meaningful search could be carried out, specifically:**

Two claims were labelled as claim 2, therefore, it was unclear what applicants intended by the second claim 2. In addition, it was not clear on which claim 2 claims 3 and 4 depended. Claims 7, 9, 10, and 14 all were dependent upon themselves. Accordingly, neither they, or the claims dependent upon them, were searchable.